

#112



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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/709,103

DATE: 04/02/2002 (3/29/02)

TIME: 09:33:08

Input Set : A:\60388-a-pu.txt

Output Set: N:\CRF3\04022002\I709103.raw

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3 <110> APPLICANT: Cismowski, Mary
4   Duzic, Emir
6 <120> TITLE OF INVENTION: AGS Proteins and Nucleic Acid Molecules and Uses Therefor
8 <130> FILE REFERENCE: 60388-A-PCT-US
10 <140> CURRENT APPLICATION NUMBER: 09/709,103
11 <141> CURRENT FILING DATE: 2000-11-08
13 <160> NUMBER OF SEQ ID NOS: 73
15 <170> SOFTWARE: PatentIn version 3.1
17 <210> SEQ ID NO: 1
18 <211> LENGTH: 846
19 <212> TYPE: DNA
20 <213> ORGANISM: Homo Sapien
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23 <221> NAME/KEY: CDS
24 <222> LOCATION: (1)..(843)
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31 1                               5                               10                               15
33 ctg agt atc ccg gcc aag aac tgc tat cgc atg gtc atc ctc ggc tcg      96
34 Leu Ser Ile Pro Ala Lys Asn Cys Tyr Arg Met Val Ile Leu Gly Ser
35 20                               25                               30
37 tcc aag gtg ggc aag acg gcc atc gtg tgc cgc ttc ctc acc ggc cgc      144
38 Ser Lys Val Gly Lys Thr Ala Ile Val Ser Arg Phe Leu Thr Gly Arg
39 35                               40                               45
41 ttc gag gac gcc tac acg cct acc atc gag gac ttc cac cgc aag ttc      192
42 Phe Glu Asp Ala Tyr Thr Pro Thr Ile Glu Asp Phe His Arg Lys Phe
43 50                               55                               60
45 tac tcc atc cgc ggc gag gtc tac cag ctc gac atc ctc gac acg tcc      240
46 Tyr Ser Ile Arg Gly Glu Val Tyr Gln Leu Asp Ile Leu Asp Thr Ser
47 65                               70                               75                               80
49 ggc aac cac ccg ttc ccc gcc atg cgg cgc ctc tcc atc ctc aca gga      288
50 Gly Asn His Pro Phe Pro Ala Met Arg Arg Leu Ser Ile Leu Thr Gly
51 85                               90                               95
53 gac gtt ttc atc ctg gtg ttc agt ctg gac aac cgc gac tcc ttc gag      336
54 Asp Val Phe Ile Leu Val Phe Ser Leu Asp Asn Arg Asp Ser Phe Glu
55 100                              105                              110
57 gag gtg cag cgg ctc agg cag cag atc ctc gac acc aag tct tgc ctc      384
58 Glu Val Gln Arg Leu Arg Gln Gln Ile Leu Asp Thr Lys Ser Cys Leu
59 115                              120                              125
61 aag aac aaa acc aag gag aac gtg gac gtg ccc ctg gtc atc tgc ggc      432
62 Lys Asn Lys Thr Lys Glu Asn Val Asp Val Pro Leu Val Ile Cys Gly

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63      130      135      140
65 aac aag ggt gac cgc gac ttc tac cgc gag gtg gac cag cgc gag atc      480
66 Asn Lys Gly Asp Arg Asp Phe Tyr Arg Glu Val Asp Gln Arg Glu Ile
67 145      150      155      160
69 gag cag ctg gtg ggc gac gac ccc cag cgc tgc gcc tac ttc gag atc      528
70 Glu Gln Leu Val Gly Asp Asp Pro Gln Arg Cys Ala Tyr Phe Glu Ile
71      165      170      175
73 tcg gcc aag aag aac agc agc ctg gac cag atg ttc cgc gcg ctc ttc
74 Ser Ala Lys Lys Asn Ser Ser Leu Asp Gln Met Phe Arg Ala Leu Phe      576
75      180      185      190
77 gcc atg gcc aag ctg ccc agc gag atg agc cca gac ctg cac cgc aag
78 Ala Met Ala Lys Leu Pro Ser Glu Met Ser Pro Asp Leu His Arg Lys      624
79      195      200      205
81 gtc tcg gtg cag tac tgc gac gtg ctg cac aag aag gcg ctg cgg aac
82 Val Ser Val Gln Tyr Cys Asp Val Leu His Lys Lys Ala Leu Arg Asn      672
83      210      215      220
85 aag aag ctg ctg cgg gcc ggc agc ggc ggc ggc ggc gac ccg ggc
86 Lys Lys Leu Leu Arg Ala Gly Ser Gly Gly Gly Gly Asp Pro Gly      720
87 225      230      235      240
89 gac gcc ttt ggc atc gtg gca ccc ttc gcg cgc cgg ccc agc gta cac
90 Asp Ala Phe Gly Ile Val Ala Pro Phe Ala Arg Arg Pro Ser Val His      768
91      245      250      255
93 agc gac ctc atg tac atc cgc gag aag gcc agc gcc ggc agc cag gcc
94 Ser Asp Leu Met Tyr Ile Arg Glu Lys Ala Ser Ala Gly Ser Gln Ala      816
95      260      265      270
97 aag gac aag gag cgc tgc gtc atc agc tag
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104 <212> TYPE: PRT
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113 Leu Ser Ile Pro Ala Lys Asn Cys Tyr Arg Met Val Ile Leu Gly Ser
114      20      25      30
117 Ser Lys Val Gly Lys Thr Ala Ile Val Ser Arg Phe Leu Thr Gly Arg
118      35      40      45
121 Phe Glu Asp Ala Tyr Thr Pro Thr Ile Glu Asp Phe His Arg Lys Phe
122      50      55      60
125 Tyr Ser Ile Arg Gly Glu Val Tyr Gln Leu Asp Ile Leu Asp Thr Ser
126 65      70      75      80
129 Gly Asn His Pro Phe Pro Ala Met Arg Arg Leu Ser Ile Leu Thr Gly
130      85      90      95
133 Asp Val Phe Ile Leu Val Phe Ser Leu Asp Asn Arg Asp Ser Phe Glu
134      100      105      110
137 Glu Val Gln Arg Leu Arg Gln Gln Ile Leu Asp Thr Lys Ser Cys Leu
138      115      120      125

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141 Lys Asn Lys Thr Lys Glu Asn Val Asp Val Pro Leu Val Ile Cys Gly
142      130      135      140
145 Asn Lys Gly Asp Arg Asp Phe Tyr Arg Glu Val Asp Gln Arg Glu Ile
146 145      150      155      160
149 Glu Gln Leu Val Gly Asp Asp Pro Gln Arg Cys Ala Tyr Phe Glu Ile
150      165      170      175
153 Ser Ala Lys Lys Asn Ser Ser Leu Asp Gln Met Phe Arg Ala Leu Phe
154      180      185      190
157 Ala Met Ala Lys Leu Pro Ser Glu Met Ser Pro Asp Leu His Arg Lys
158      195      200      205
161 Val Ser Val Gln Tyr Cys Asp Val Leu His Lys Lys Ala Leu Arg Asn
162      210      215      220
165 Lys Lys Leu Leu Arg Ala Gly Ser Gly Gly Gly Gly Gly Asp Pro Gly
166 225      230      235      240
169 Asp Ala Phe Gly Ile Val Ala Pro Phe Ala Arg Arg Pro Ser Val His
170      245      250      255
173 Ser Asp Leu Met Tyr Ile Arg Glu Lys Ala Ser Ala Gly Ser Gln Ala
174      260      265      270
177 Lys Asp Lys Glu Arg Cys Val Ile Ser
178      275      280
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182 <211> LENGTH: 1801
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187 <221> NAME/KEY: CDS
188 <222> LOCATION: (154)..(996)
189 <223> OTHER INFORMATION:
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195 ccagccgctc accccgcgtg ccacccagc gaccctcagc cgctctctgc ccttctctcg 120
197 gccccgcgcc cgccctcgcg gccctctgca cca atg aaa ctg gcc gcg atg atc 174
198      Met Lys Leu Ala Ala Met Ile
199      1      5
201 aag aag atg tgc ccg agc gac tcg gag ctg agt atc ccg gcc aag aac 222
202 Lys Lys Met Cys Pro Ser Asp Ser Glu Leu Ser Ile Pro Ala Lys Asn
203      10      15      20
205 tgc tat cgc atg gtc atc ctc ggc tcg tcc aag gtg ggc aag acg gcc 270
206 Cys Tyr Arg Met Val Ile Leu Gly Ser Ser Lys Val Gly Lys Thr Ala
207      25      30      35
209 atc gtg tcg cgc ttc ctc acc ggc cgc ttc gag gac gcc tac acg cct 318
210 Ile Val Ser Arg Phe Leu Thr Gly Arg Phe Glu Asp Ala Tyr Thr Pro
211 40      45      50      55
213 acc atc gag gac ttc cac cgc aag ttc tac tcc atc cgc ggc gag gtc 366
214 Thr Ile Glu Asp Phe His Arg Lys Phe Tyr Ser Ile Arg Gly Glu Val
215      60      65      70
217 tac cag ctc gac atc ctc gac acg tcc ggc aac cac ccg ttc ccc gcc 414
218 Tyr Gln Leu Asp Ile Leu Asp Thr Ser Gly Asn His Pro Phe Pro Ala
219      75      80      85

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221	atg	cgg	cgc	ctc	tcc	atc	ctc	aca	gga	gac	gtt	ttc	atc	ctg	gtg	ttc	462
222	Met	Arg	Arg	Leu	Ser	Ile	Leu	Thr	Gly	Asp	Val	Phe	Ile	Leu	Val	Phe	
223		90						95				100					
225	agt	ctg	gac	aac	cgc	gac	tcc	ttc	gag	gag	gtg	cag	cgg	ctc	agg	cag	
226	Ser	Leu	Asp	Asn	Arg	Asp	Ser	Phe	Glu	Glu	Val	Gln	Arg	Leu	Arg	Gln	510
227		105						110				115					
229	cag	atc	ctc	gac	acc	aag	tct	tgc	ctc	aag	aac	aaa	acc	aag	gag	aac	
230	Gln	Ile	Leu	Asp	Thr	Lys	Ser	Cys	Leu	Lys	Asn	Lys	Thr	Lys	Glu	Asn	558
231	120							125				130					
233	gtg	gac	gtg	ccc	ctg	gtc	atc	tgc	ggc	aac	aag	ggt	gac	cgc	gac	ttc	
234	Val	Asp	Val	Pro	Leu	Val	Ile	Cys	Gly	Asn	Lys	Gly	Asp	Arg	Asp	Phe	606
235				140								145					
237	tac	cgc	gag	gtg	gac	cag	cgc	gag	atc	gag	cag	ctg	gtg	ggc	gac	gac	
238	Tyr	Arg	Glu	Val	Asp	Gln	Arg	Glu	Ile	Glu	Gln	Leu	Val	Gly	Asp	Asp	654
239				155								160					
241	ccc	cag	cgc	tgc	gcc	tac	ttc	gag	atc	tcg	gcc	aag	aag	aac	agc	agc	
242	Pro	Gln	Arg	Cys	Ala	Tyr	Phe	Glu	Ile	Ser	Ala	Lys	Lys	Asn	Ser	Ser	702
243				170								175					
245	ctg	gac	cag	atg	ttc	cgc	gcg	ctc	ttc	gcc	atg	gcc	aag	ctg	ccc	agc	
246	Leu	Asp	Gln	Met	Phe	Arg	Ala	Leu	Phe	Ala	Met	Ala	Lys	Leu	Pro	Ser	750
247				185								190					
249	gag	atg	agc	cca	gac	ctg	cac	cgc	aag	gtc	tcg	gtg	cag	tac	tgc	gac	
250	Glu	Met	Ser	Pro	Asp	Leu	His	Arg	Lys	Val	Ser	Val	Gln	Tyr	Cys	Asp	798
251	200							205				210					
253	gtg	ctg	cac	aag	aag	gcg	ctg	cgg	aac	aag	aag	ctg	ctg	cgg	gcc	ggc	
254	Val	Leu	His	Lys	Lys	Ala	Leu	Arg	Asn	Lys	Lys	Leu	Leu	Arg	Ala	Gly	846
255						220						225					
257	agc	ggc	ggc	ggc	ggc	ggc	gac	ccg	ggc	gac	gcc	ttt	ggc	atc	gtg	gca	
258	Ser	Gly	Gly	Gly	Gly	Gly	Asp	Pro	Gly	Asp	Ala	Phe	Gly	Ile	Val	Ala	894
259				235								240					
261	ccc	ttc	gcg	cgc	cgg	ccc	agc	gta	cac	agc	gac	ctc	atg	tac	atc	cgc	
262	Pro	Phe	Ala	Arg	Arg	Pro	Ser	Val	His	Ser	Asp	Leu	Met	Tyr	Ile	Arg	942
263				250								255					
265	gag	aag	gcc	agc	gcc	ggc	agc	cag	gcc	aag	gac	aag	gag	cgc	tgc	gtc	
266	Glu	Lys	Ala	Ser	Ala	Gly	Ser	Gln	Ala	Lys	Asp	Lys	Glu	Arg	Cys	Val	990
267				265								270					
269	atc	agc	taggagcccc	gcccgcgtgg	cgacacaacc	taaggaggac	ctttttgtta					275					
270	Ile	Ser															1046
271	280																
273	agtcaaatcc	aacggccccg	tgccgcccag	gcccgggagcg	cgcgcggact	ggcgtctccc											
275	ctcccggcga	tccgccccca	gcactgggga	ggcgccactg	aaccgagaag	ggacgggtcat											1106
277	ctgctccgga	aggaaagaga	acggggccaag	actgggacta	ttccccaccc	ccggtcccc											1166
279	attgaggccc	gccaccccc	taactttggg	agcgagggcc	cagccgaggg	tggatttacc											1226
281	ttctcaaaga	cctaagagtg	agcgcggggt	gggggagggga	tgtgaagtta	tccagcctct											1286
283	gctaggcttc	aagaaaccgt	catgcccgc	tgagggtcag	gacccacggg	gcattatott											1346
285	gtctgtgatt	ccgggttgct	gtgacagccg	gtagagcctc	tgcctcccc	aaactaagcg											1406
287	ggggggcggtg	ggtcaaatca	tagccaagt	acttggttac	atgtgagtga	aactgcacaa											1466
289	aggaacacaa	aacaaaactt	gcactttaac	ggtagttccg	gtgtcaacat	ggacaogaac											1526
291	aaaacettac	ccagggtgttt	atactgtgtg	tgtgtgaggt	ctttaaagtt	attgctttat											1586
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293 ttggtttttt aatatacaat aaaataattt aaaatggaaa aaaaaaaaaa aaaaaaaaaa 1706
295 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aagcggccgc tcgagcatgc 1766
297 atctagaggg ccgcatcatg taattagtta tgaac 1801
300 <210> SEQ ID NO: 4
301 <211> LENGTH: 281
302 <212> TYPE: PRT
303 <213> ORGANISM: Homo Sapien
305 <400> SEQUENCE: 4
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312 20 25 30
315 Ser Lys Val Gly Lys Thr Ala Ile Val Ser Arg Phe Leu Thr Gly Arg
316 35 40 45
319 Phe Glu Asp Ala Tyr Thr Pro Thr Ile Glu Asp Phe His Arg Lys Phe
320 50 55 60
323 Tyr Ser Ile Arg Gly Glu Val Tyr Gln Leu Asp Ile Leu Asp Thr Ser
324 65 70 75 80
327 Gly Asn His Pro Phe Pro Ala Met Arg Arg Leu Ser Ile Leu Thr Gly
328 85 90 95
331 Asp Val Phe Ile Leu Val Phe Ser Leu Asp Asn Arg Asp Ser Phe Glu
332 100 105 110
335 Glu Val Gln Arg Leu Arg Gln Gln Ile Leu Asp Thr Lys Ser Cys Leu
336 115 120 125
339 Lys Asn Lys Thr Lys Glu Asn Val Asp Val Pro Leu Val Ile Cys Gly
340 130 135 140
343 Asn Lys Gly Asp Arg Asp Phe Tyr Arg Glu Val Asp Gln Arg Glu Ile
344 145 150 155 160
347 Glu Gln Leu Val Gly Asp Asp Pro Gln Arg Cys Ala Tyr Phe Glu Ile
348 165 170 175
351 Ser Ala Lys Lys Asn Ser Ser Leu Asp Gln Met Phe Arg Ala Leu Phe
352 180 185 190
355 Ala Met Ala Lys Leu Pro Ser Glu Met Ser Pro Asp Leu His Arg Lys
356 195 200 205
359 Val Ser Val Gln Tyr Cys Asp Val Leu His Lys Lys Ala Leu Arg Asn
360 210 215 220
363 Lys Lys Leu Leu Arg Ala Gly Ser Gly Gly Gly Gly Asp Pro Gly
364 225 230 235 240
367 Asp Ala Phe Gly Ile Val Ala Pro Phe Ala Arg Arg Pro Ser Val His
368 245 250 255
371 Ser Asp Leu Met Tyr Ile Arg Glu Lys Ala Ser Ala Gly Ser Gln Ala
372 260 265 270
375 Lys Asp Lys Glu Arg Cys Val Ile Ser
376 275 280
379 <210> SEQ ID NO: 5
380 <211> LENGTH: 54
381 <212> TYPE: DNA
382 <213> ORGANISM: Artificial Sequence
384 <220> FEATURE:

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VERIFICATION SUMMARY

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Input Set : A:\60388-a-pu.txt

Output Set: N:\CRF3\04022002\I709103.raw

L:557 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18
L:577 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19
L:597 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20
L:617 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:643 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22